

Microbiological Characteristics of Community-Acquired Pneumonia in Children in Northern Vietnam

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Abstract

Background: This study aimed to identify the distribution of bacteria causing community-acquired pneumonia (CAP) among inpatients at the Respiratory Department of Hai Phong Children's Hospital and their antibiotic-resistance properties.

Methods and Results: This study analyzed data of 653 inpatients aged 2 months to under 15 years diagnosed with CAP according to WHO criteria recruited from May 1, 2022, to April 30, 2023. The most common bacterial causes of CAP in hospitalized children were *Haemophilus influenzae*, followed by *Streptococcus pneumoniae* (25.7%), *Moraxella catarrhalis* (12.6%), and *Staphylococcus aureus* (1.4%). We also found that the most commonly used first-line antibiotics for CAP, such as cephalosporins and broad-spectrum penicillins, were the least effective against these pathogens. Almost all the four types of bacteria tested (*H. influenzae*, *S. pneumoniae*, *M. catarrhalis*, and *S. aureus*) were found to be multidrug-resistant.

Conclusion: The antibiogram results showed that antibiotic resistance is increasing alarmingly, particularly for first-line antibiotics. Almost all the isolates were multidrug-resistant. (**International Journal of Biomedicine. 2025;15(1):183-187.**)

Keywords: children • community-acquired pneumonia • first-line antibiotics • antibiotic resistance • multidrug resistance

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Introduction

Community-acquired pneumonia (CAP) is an acute infection of the lung parenchyma acquired outside of hospitals or other healthcare settings.¹ It is one of the most common causes of hospitalization among children in developed countries² and the leading cause of death among children in developing countries.³ Vietnam is one of the 15 countries in the world with the highest number of children suffering from pneumonia, with around 2.9 million children affected and around 4,000 children dying from pneumonia each year—10 times more than in developed countries.⁴ A definitive diagnosis of CAP is often challenging because symptoms vary with age and may be nonspecific in young children. Furthermore, determining the etiology of CAP remains a significant challenge.¹ Antibiotic resistance is an inevitable consequence of antibiotic use in treatment and is particularly increasing as the misuse of antibiotics becomes more prevalent.⁵ Nasopharyngeal culture remains a common test for determining the type of bacteria present in CAP, and it can be combined with susceptibility testing to study their antibiotic-resistance characteristics. Variations in antibiotic-resistance patterns and the effectiveness of interventions are critical

aspects of the complex global problem of antibiotic resistance. These variations are influenced by multiple factors, including geographic location, healthcare practices, socioeconomic conditions, and the implementation of intervention strategies.⁶

This study aimed to identify the distribution of bacteria causing CAP among inpatients at the Respiratory Department of Hai Phong Children's Hospital and their antibiotic-resistance properties.

Materials and Methods

This was a descriptive study of a series of cases. We used a database containing all electronic medical records of patients hospitalized for CAP, recruited from the Respiratory Department of Hai Phong Children's Hospital (Haiphong, Vietnam), from May 1, 2022, to April 30, 2023.

Inclusion criteria: Electronic medical records of patients aged 2 months to under 15 years diagnosed with CAP according to WHO criteria:⁷ cough, tachypnea or dyspnea; crackles, bronchial breathing or auscultation.

Exclusion criteria: Electronic medical records lacking sufficient necessary data; patients with underlying comorbidities, such as immunodeficiency, tuberculosis,

chronic disease or chest problems; and patients with ventilator-associated pneumonia.

Extracted laboratory measurements included Gram stain and culture. A microbiological test based on the culture results of nasopharyngeal swab samples was conducted in the hospital's microbiology laboratory from the start of the patient's hospitalization. The bacterial culture and identification technique in the automated system used a nutrient-rich agar plate environment to cultivate and isolate bacteria from nasopharyngeal fluid samples. After cultivation, the bacteria were incubated at 35°C–37°C for 18–24 hours (routine), or 48–72 hours for difficult-to-culture bacteria. Bacteria were identified based on the morphology of the culture. We used tests to identify basic biological and chemical properties such as oxidase, catalase, etc. The system VITEK® 2 COMPACT was applied to automatically determine the biological and chemical properties to identify pathogenic bacteria.⁸ The antibiogram of the identified bacterial isolates was carried out using the Kirby-Bauer disk diffusion susceptibility test.^{9,10}

A convenient sampling method, including all medical records of patients meeting the selection criteria, was used for this study. The following parameters were recorded: month of admission, age, sex, type of bacteria, and antibiogram results.

Results

A total of 653 cases were analyzed in this study. The most common bacteria causing CAP in our study were *Haemophilus influenzae*, followed by *Streptococcus pneumoniae* (25.7%), *Moraxella catarrhalis* (12.6%), and *Staphylococcus aureus* (1.4%) (Fig. 1A). There was no significant difference in the distribution of pathogenic bacteria across age groups. *H. influenzae* remained the most common bacterium in children aged 2 months to <15 years admitted to our hospital. *S. pneumoniae* and *S. aureus* were the second most common etiologies in the 2-month to 5-year and >5-year groups, respectively (Fig. 1B, C, and D). *H. influenzae* exhibited the highest rate from January to April, which corresponds to winter in Northern Vietnam. *M. catarrhalis* had the highest rate in November–January (Fig. 2).

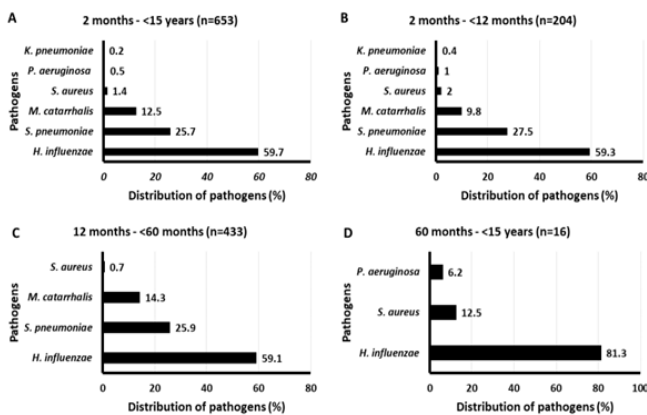


Fig. 1. Bacterial pathogens responsible for CAP in children. The distribution of bacterial pathogens of CAP in children in this study (A) and in each age group (B, C and D).

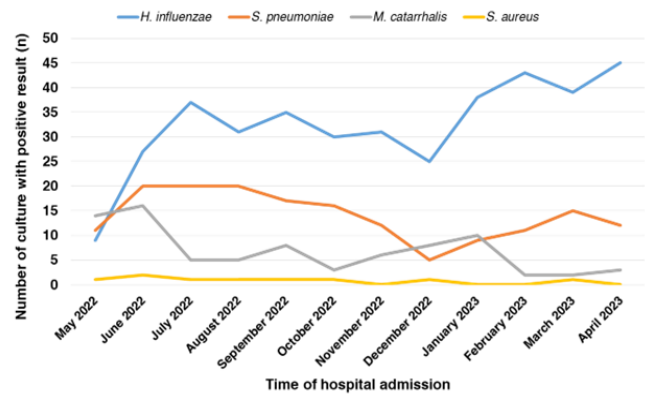


Fig. 2. Distribution of the most frequent pathogens of CAP according to the time of hospital admission.

The distribution of pathogenic isolates in children with CAP by time of diagnosis showed a decrease in the number of positive cultures between November and December, followed by an increase in cases in early 2023.

We assessed *in vitro* antibiotic resistance of the four major causative bacteria found in children with CAP using an antibiogram of the pathogens identified from the patient's nasopharyngeal swab samples. Rates of antibiotic resistance varied considerably depending on etiologies. The major bacterial species causing CAP exhibited substantial rates of resistance to several antibiotics widely used in clinical practice.

H. influenzae was highly resistant to penicillin antibiotics (including ampicillin and ampicillin/sulbactam), macrolides, and cotrimoxazole, except for amoxicillin/clavulanic acid, which had an average resistance rate of 53.9%. *H. influenzae* showed low rates of resistance to third-generation cephalosporin and carbapenem antibiotics (Table 1).

Table 1.

Characteristics of *in vitro* antibiotic resistance of *H. influenzae* inducing CAP in children (n = 390)

Antibiotic	Number of test	S (%)	I (%)	R (%)
Ampicillin	194	1.0	0.0	99.0
Amox/clavu*	267	46.1	0.0	53.9
Cefuroxime	355	2.3	0.0	97.7
Ceftazidime	388	83.8	0.0	16.2
Cefotaxime	367	85.8	0.0	14.2
Ceftriaxone	303	89.1	0.0	10.9
Cefepime	302	42.4	0.0	57.6
Ampi/sulba**	378	6.1	0.0	93.9
Azithromycin	259	10.4	0.0	89.6
Ciprofloxacin	341	93.8	0.0	6.2
Imipenem	344	93.6	0.0	6.4
Meropenem	350	98.6	0.0	1.4
Cotrimoxazole	218	3.2	0.9	95.9
Piper/tazo***	295	100.0	0.0	0.0

(*): amoxicillin/clavulanic acid; (**): ampicillin/sulbactam; (***): piperacillin/tazobactam

S. pneumoniae was identified from the patient's nasopharyngeal sample and exhibited high resistance to many antibiotics, particularly macrolides (98%) and trimethoprim/sulfamethoxazole (91.7%). *S. pneumoniae* was also susceptible to antibiotics recommended for the treatment of CAP, such as amoxicillin/clavulanic acid, ceftriaxone, cefotaxime, carbapenems, and vancomycin (Table 2). *M. catarrhalis* demonstrated strong resistance to most antibiotics tested in the antibiogram, including cefuroxime, azithromycin, erythromycin, and cotrimoxazole. *M. catarrhalis* showed high susceptibility to amoxicillin/clavulanic acid (100%) and ciprofloxacin (93/7%) (Table 3).

Table 2.

Characteristics of in vitro antibiotic resistance of *S. pneumoniae* inducing CAP in children (n = 168)

Antibiotic	Number of test	S (%)	I (%)	R (%)
Amox/clavu*	133	94.0	0.0	6.0
Oxacillin	136	0.7	0.0	99.3
Cefuroxime	164	54.9	0.0	45.1
Cefotaxime	159	94.3	0.0	5.7
Ceftriaxone	146	95.9	0.0	4.1
Cefepime	131	91.6	0.0	8.4
Azithromycin	130	1.5	0.0	98.5
Erythromycin	163	1.2	0.0	98.8
Imipenem	158	99.4	0.0	0.6
Meropenem	162	98.1	0.0	1.9
Cotrimoxazole	84	4.8	3.6	91.6
Clindamycin	157	4.5	0.0	95.5
Vancomycin	165	99.4	0.0	0.6
Levofloxacin	163	96.9	0.0	3.1

(*): amoxicillin/clavulanic acid

Table 3.

Characteristics of in vitro antibiotic resistance of *M. catarrhalis* inducing CAP in children (n = 82)

Antibiotic	Number of test	S (%)	I (%)	R (%)
Amox/clavu*	77	100.0	0.0	0.0
Cefuroxime	82	0.0	26.8	73.2
Azithromycin	63	4.8	1.6	93.6
Erythromycin	81	8.6	1.2	90.2
Ciprofloxacin	79	93.7	0.0	6.3
Cotrimoxazole	63	11.1	0.0	88.9

(*): amoxicillin/clavulanic acid

Multidrug-resistant bacteria were identified when the bacterial isolate was found to be resistant to three or more types of antibiotics. Most isolates of pathogenic bacteria causing CAP in children are multidrug-resistant (Table 4).

Table 4.

Multi-drug resistance in bacterial pathogens causing CAP in children.

Bacterial isolates	Resistance level							Total ≥ R3
	R0	R1	R2	R3	R4	R5	≥ R6	
<i>H. influenzae</i>	0	2	7	34	77	60	80	251/260 (96.5%)
<i>S. pneumoniae</i>	0	0	3	22	52	45	31	150/153 (98%)
<i>M. catarrhalis</i>	2	4	10	38	23	4	0	65/81 (80.2%)
<i>S. aureus</i>	0	1	0	1	0	2	9	12/13 (92.3%)

Discussion

Bacteria were detected in 43.2% of nasopharyngeal swab culture samples. Notably, *H. influenzae* was the most common bacterial pathogen in all age groups in our study (59.6%). *S. pneumoniae* (25.7%) was identified as the second most common etiology in children aged 2 months to 5 years. Our study's findings are consistent with previous research, indicating that the most common organisms causing CAP in children are *H. influenzae* and *S. pneumoniae*. For example, in a study by Honkinen et al. in Finland, *S. pneumoniae* (50%) was the most prevalent etiology, followed by *H. influenzae* (38%).¹² Similarly, research conducted in Singapore found *S. pneumoniae* to be the most common pathogen causing pneumonia in children (46.6%), followed by *H. influenzae* (21.7%).¹³

Meanwhile, in children over 5, the most common pathogen was *H. influenzae* (81.3%). This high rate of *H. influenzae* might be a remarkable change in CAP pathogens as we observed in our study just after the COVID-19 pandemic in Vietnam. It should be noted that studies conducted prior to the pandemic indicated that *Mycoplasma pneumoniae* frequently occurred in children aged 5 to 13 years;¹⁴ however, *S. pneumoniae* remained the commonly identified organism.¹⁵ The limitation of nasopharyngeal swab culture is that it cannot detect atypical viruses and bacteria that also cause CAP in children. As a result, cases of *Mycoplasma pneumoniae* were not included in our study. Further research is needed to verify the increased rate of *H. influenzae* among CAP-inducing pathogens in children, particularly in those older than 5 years.

Our study on the seasonal distribution of CAP pathogens revealed a monthly prevalence of bacterial infections. To exclude the period affected by the local impact of COVID-19, we conducted the study from May 2022 to April 2023. The distribution of CAP pathogenic isolates in children, based on the time of diagnosis, showed a decrease in the number of positive cultures between November 2022 and December 2022, followed by an increase in cases in early 2023. It should be noted that during winter, when children are more likely to stay indoors, close contact increases the transmission of pathogens.¹⁶

The results of this study demonstrated that *H. influenzae* was highly resistant to penicillin (including ampicillin and ampicillin/sulbactam), macrolides, and cotrimoxazole antibiotics, except for amoxicillin/clavulanic acid, which showed a moderate resistance rate. *H. influenzae* exhibited

low resistance rates to third-generation cephalosporins and carbapenem antibiotics. Our findings on *H. influenzae* antibiotic resistance were consistent with a recent study on antimicrobial resistance of isolates from pediatric hospitals in mainland China, which showed that more than 90% of *H. influenzae* isolates were susceptible to ceftriaxone, cefotaxime, meropenem, levofloxacin, and chloramphenicol. The resistance rates to ampicillin and azithromycin in *H. influenzae* have shown an increasing trend over the years.¹⁷

S. pneumoniae was identified from the patient's nasopharyngeal specimen, revealing high resistance to many types of antibiotics, particularly macrolides and cotrimoxazole. However, *S. pneumoniae* was susceptible to antibiotics recommended for the treatment of CAP, such as amoxicillin/clavulanic acid, ceftriaxone, and cefotaxime. In agreement with our findings, Sunakawa and Farrell¹⁸ found that *S. pneumoniae* isolates were highly resistant to azithromycin and erythromycin (75.4% and 77.8%, respectively), while susceptibility to amoxicillin and clavulanic acid was 99.6%. Our study also showed that *S. pneumoniae* was susceptible to antibiotics recommended for the treatment of severe cases of CAP, such as carbapenems and vancomycin, which is consistent with the observation of current studies.¹⁹⁻²¹

M. catarrhalis was found to have high resistance to most antibiotics used in antibiograms, including cefuroxime, azithromycin, erythromycin and cotrimoxazole. However, *M. catarrhalis* showed high susceptibility to amoxicillin/clavulanic acid and ciprofloxacin. A study by Tabassum in Pakistan reported that 95% of *M. catarrhalis* strains were susceptible to ciprofloxacin.²² Our results were like those of Shaikh et al.,²³ who found that the resistance to amoxicillin/clavulanic acid was only 4%. Another study in a semi-arid region of Western Australia showed that a large proportion of *M. catarrhalis* strains were resistant to ampicillin and/or cotrimoxazole.²⁴

The main challenge in the treatment of bacterial infections is their resistance to antibiotics, often reported as multidrug resistance (resistance to at least one agent in three or more antibiotic classes).^{25,26} This resistance makes the clinical management of pneumonia caused by such pathogens difficult for physicians. Pneumonia is one of the most commonly treated diseases with antibiotic therapy worldwide, accounting for 19% of patients treated. The most commonly prescribed antibiotics for nosocomial infections are penicillin with a β -lactamase inhibitor, amoxicillin with a β -lactamase inhibitor, and piperacillin with a β -lactamase inhibitor. Third-generation cephalosporins, particularly ceftriaxone, followed by fluoroquinolones, are the second most commonly prescribed antibiotics for nosocomial infections.²⁷ It is noteworthy that in our study, nearly all four types of bacteria tested (*H. influenzae*, *S. pneumoniae*, *M. catarrhalis*, and *S. aureus*) have been found to be multidrug-resistant. These results underscore the need for strict monitoring and various measures to reduce the development of multidrug resistance and to design more effective strategies to control its spread, as suggested by the European Antimicrobial Resistance Surveillance Network.²⁸

In summary, our study showed that the most common bacterial causes of CAP in hospitalized children were *H.*

influenzae, *S. pneumoniae*, and *M. catarrhalis*, respectively. We also found that the most commonly used first-line antibiotics for CAP, such as cephalosporins and broad-spectrum penicillins, were the least effective against these pathogens. Almost all the four types of bacteria tested (*H. influenzae*, *S. pneumoniae*, *M. catarrhalis*, and *S. aureus*) were found to be multidrug-resistant.

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Competing Interests

The authors declare that they have no competing interests.

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